Figure 1A
TR-11

```
  1   GCACTTCACCTGGGTCGGGATTCTCAGGTCATGAACGGTCCCAGCCACCTCCGGGCAGGG    60

 61   CGGGTGAGGACGGGGACGGGGCGTGTCCAACTGGCTGTGGGCTCTTGAAACCCGAGCATG   120
  1                                                              M      1

121   GCACAGCACGGGGCGATGGGCGCGTTTCGGGCCCTGTGCGGCCTGGCGCTGCTGTGCGCG   180
  2   A  Q  H  G  A  M  G  A  F  R  A  L  C  G  L  A  L  L  C  A      21

181   CTCAGCCTGGGTCAGCGCCCCACCGGGGGTCCCGGGTGCGGCCCTGGGCGCCTCCTGCTT   240
 22   L  S  L  G  Q  R  P  T  G  G  P  G  C  G  P  G  R  L  L         41

241   GGGACGGGAACGGACGCGCGCTGCTGCCGGGTTCACACGACGCGCTGCTGCCGCGATTAC   300
 42   G  T  G  T  D  A  R  C  C  R  V  H  T  T  R  C  C  R  D  Y      61

301   CCGGGCGAGGAGTGCTGTTCCGAGTGGGACTGCATGTGTGTCCAGCCTGAATTCCACTGC   360
 62   P  G  E  E  C  C  S  E  W  D  C  M  C  V  Q  P  E  F  H  C      81
                                     CD-II

361   GGAGACCCTTGCTGCACGACCTGCCGGCACCACCCTTGTCCCCCAGGCCAGGGGGTACAG   420
 82   G  D  P  C  C  T  T  C  R  H  H  P  C  P  P  G  Q  G  V  Q     101
                  CD-III

421   TCCCAGGGGAAATTCAGTTTTTGGCTTCCAGTGTATCGACTGTGCCTCGGGGACCTTCTCC   480
102   S  Q  G  K  F  S  F  G  F  Q  C  I  D  C  A  S  G  T  F  S     121
                     CD-IV

481   GGGGGCCACGAAGGCCACTGCAAACCTTGGACAGACTGCACCCAGTTCGGGTTTCTCACT   540
122   G  G  H  E  G  H  C  K  P  W  T  D  C  T  Q  F  G  F  L  T     141
                        CD-V

541   GTGTTCCCTGGGAACAAGACCCACAACGCTGTGTGCGTCCCAGGGTCCCCGCCGGCAGAG   600
142   V  F  P  G  N  K  T  H  N  A  V  C  V  P  G  S  P  P  A  E     161
                                    CD-VI

601   CCGCTTGGGTGGCTGACCGTCGTCCTCCTGGCCGTGGCCGCCTGCGTCCTCCTCCTGACC   660
162   P  L  G  W  L  T  V  V  L  L  A  V  A  A  C  V  L  L  L  T     181
                                         CD-VII

661   TCGGCCCAGCTTGGACTGCACATCTGGCAGCTGAGGAAGACCCAGCTGCTGCTGGAGGTG   720
182   S  A  Q  L  G  L  H  I  W  Q  L  R  K  T  Q  L  L  L  E  V     201
        CD-VII

721   CCGCCGTCGACCGAAGACGCCAGAAGCTGCCAGTTCCCCGAGGAAGAGCGGGGCGAGCGA   780
202   P  P  S  T  E  D  A  R  S  C  Q  F  P  E  E  E  R  G  E  R     221
           CD-IX

781   TCGGCAGAGGAGAAGGGGCGGCTGGGAGACCTGTGGGTGTGAGCCTGGCCGTCCTCCGGG   840
222   S  A  E  E  K  G  R  L  G  D  L  W  V                         234
           CD-X

841   GCCACCGACCGCAGCCAGCCCCTCCCCAGGAGCTCCCCAGGCCGCAGGGGCTCTGCGTTC   900
```

Figure 1B
TR-11

901 TGCTCTGGGCCGGGCCCTGCTCCCCTGGCAGCAGAAGTGGGTGCAGGAAGGTGGCAGTGA 960

961 CCAGCGCCCTGGACCATGCAGTT 983

```
  1  GTCGACCCACGCGTCCGGGGGGCCACCCCTGGGTCCTGCAGGGGCAGCTCCTGGTTGCAT   60


 61  ATGGAGTTAGCACCTGGGCAGGGGCAGCTGTGGGGCGCAAAGGGGGAGTAGCCAGGCCAC  120


121  ATGGCCCCAGGAGAAAGAGACAGCTGGATAAACCCAGGTCCAGACTCCCAGCCAGGAGCC  180
  1   M   A   P   G   E   R   D   S   W   I   N   P   G   P   D   S   Q   P   G   A    20


181  CTCTGCTCCCTGGAGCCAACTGTGGGTGGAGAACGGACAACCTCACTCCCCTGGAGGGCC  240
 21   L   C   S   L   E   P   T   V   G   G   E   R   T   T   S   L   P   W   R   A    40


241  GAGGGGAGGCCTGGGGAGGAGGGGGCCTCAGCCCAGCTGCTGGGGGGCTGGCCTGTCTCC  300
 41   E   G   R   P   G   E   E   G   A   S   A   Q   L   L   G   G   W   P   V   S    60
                                        ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾
                                                  CD-I

301  TGCCCAGGCGAGGAGTGCTGTTCCGAGTGGGACTGCATGTGTGTCCAGCCTGAATTCCAC  360
 61   C   P   G   E   E   C   C   S   E   W   D   C   M   C   V   Q   P   E   F   H    80
      ‾                                     ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾
                                                      CD-II

361  TGCGGAGACCCTTGCTGCACGACCTGCCGGCACCACCCTTGTCCCCCAGGCCAGGGGGTA  420
 81   C   G   D   P   C   C   T   T   C   R   H   H   P   C   P   P   G   Q   G   V   100
      ‾           ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾
    CD-II                   CD-III

421  CAGTCCCAGGGGAAATTCAGTTTTGGCTTCCAGTGTATCGACTGTGCCTCGGGGACCTTC  480
101   Q   S   Q   G   K   F   S   F   G   F   Q   C   I   D   C   A   S   G   T   F   120
                          ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾
                                   CD-IV

481  TCCGGGGGGCCACGAAGGCCACTGCAAACCTTGGACAGACTGCACCCAGTTCGGGTTTCTC  540
121   S   G   G   H   E   G   H   C   K   P   W   T   D   C   T   Q   F   G   F   L   140
                              ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾
                                       CD-V
                                 #
541  ACTGTGTTCCCTGGGAACAAGACCCACAACGCTGTGTGCGTCCCAGGGTCCCCGCCGGCA  600
141   T   V   F   P   G   N   K   T   H   N   A   V   C   V   P   G   S   P   P   A   160
                                          ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾
                                                   CD-VI

601  GAGCCGCTTGGGTGGCTGACCGTCGTCCTCCTGGCCGTGGCCGCCTGCGTCCTCCTCCTG  660
161   E   P   L   G   W   L   T   V   V   L   L   A   V   A   A   C   V   L   L   L   180
                                                      ‾‾‾‾‾‾‾‾‾‾‾‾‾
                                                          CD-VII

661  ACCTCGGCCCAGCTTGGACTGCACATCTGGCAGCTGAGGAGTCAGTGCATGTGGCCCCGA  720
181   T   S   A   Q   L   G   L   H   I   W   Q   L   R   S   Q   C   M   W   P   R   200
      ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾                           ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾
           CD-VII                                      CD-VIII

721  GAGACCCAGCTGCTGCTGGAGGTGCCGCCGTCGACCGAAGACGCCAGAAGCTGCCAGTTC  780
201   E   T   Q   L   L   L   E   V   P   P   S   T   E   D   A   R   S   C   Q   F   220
      ‾                               ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾
    CD-VIII                                  CD-IX

781  CCCGAGGAAGAGCGGGGCGAGCGATCGGCAGAGGAGAAGGGGCGGCTGGGAGACCTGTGG  840
221   P   E   E   E   R   G   E   R   S   A   E   E   K   G   R   L   G   D   L   W   240
                                          ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾
                                                   CD-X

841  GTGTGAGCCTGGCCGTCCTCCGGGGGCCACCGACCGCAGCCAGCCCCTCCCCAGGAGCTCC  900
241   V                                                            241
```

Figure 2B
TR-11SV1

901   CCAGGCCGCAGGGGCTCTGCGTTCTGCTCTGGGCCGGGCCCTGCTCCCCTGGCAGCAGAA   960

961   GTGGGTGCAGGAAGGTGGCAGTGACCAGCGCCCTGGACCATGCAGTT   1007

```
  1  ATGGGCGCGTTTCGGGCCCTGTGCGGCCTGGCGCTGCTGTGCGCGCTCAGCCTGGGTCAG   60
  1  M  G  A  F  R  A  L  C  G  L  A  L  L  C  A  L  S  L  G  Q    20


 61  CGCCCCACCGGGGGTCCCGGGTGCGGCCCTGGGCGCCTCCTGCTTGGGACGGGAACGGAC  120
 21  R  P  T  G  G  P  G  C  G  P  G  R  L  L  L  G  T  G  T  D    40


121  GCGCGCTGCTGCCGGGTTCACACGACGCGCTGCTGCCGCGATTACCCGGCCCAGCTGCTG  180
 41  A  R  C  C  R  V  H  T  T  R  C  C  R  D  Y  P  A  Q  L  L    60
                                                        CD-I


181  GGGGGCTGGCCTGTCTCCTGCCCAGGCGAGGAGTGCTGTTCCGAGTGGGACTGCATGTGT  240
 61  G  G  W  P  V  S  C  P  G  E  E  C  C  S  E  W  D  C  M  C    80
          CD-I                                           CD-II


241  GTCCAGCCTGAATTCCACTGCGGAGACCCTTGCTGCACGACCTGCCGGCACCACCCTTGT  300
 81  V  Q  P  E  F  H  C  G  D  P  C  C  T  T  C  R  H  H  P  C   100
          CD-II                       CD-III


301  CCCCCAGGCCAGGGGGGTACAGTCCCAGGGGAAATTCAGTTTTGGCTTCCAGTGTATCGAC  360
101  P  P  G  Q  G  V  Q  S  Q  G  K  F  S  F  G  F  Q  C  I  D   120
                                          CD-IV


361  TGTGCCTCGGGGACCTTCTCCGGGGGGCCACGAAGGCCACTGCAAACCTTGGACAGACTGC  420
121  C  A  S  G  T  F  S  G  G  H  E  G  H  C  K  P  W  T  D  C   140
     CD-IV                                  CD-V

                                                   #
421  ACCCAGTTCGGGTTTCTCACTGTGTTCCCTGGGAACAAGACCCACAACGCTGTGTGCGTC  480
141  T  Q  F  G  F  L  T  V  F  P  G  N  K  T  H  N  A  V  C  V   160
                                                          CD-VI


481  CCAGGGTCCCCGCCGGCAGAGCCGCTTGGGTGGCTGACCGTCGTCCTCCTGGCCGTGGCC  540
161  P  G  S  P  P  A  E  P  L  G  W  L  T  V  V  L  L  A  V  A   180
         CD-VI


541  GCCTGCGTCCTCCTCCTGACCTCGGCCCAGCTTGGACTGCACATCTGGCAGCTGAGGAAG  600
181  A  C  V  L  L  L  T  S  A  Q  L  G  L  H  I  W  Q  L  R  K   200
         CD-VII


601  ACCCAGCTGCTGCTGGAGGTGCCGCCGTCGACCGAAGACGCCAGAAGCTGCCAGTTCCCC  660
201  T  Q  L  L  L  E  V  P  P  S  T  E  D  A  R  S  C  Q  F  P   220
                             CD-IX


661  GAGGAAGAGCGGGGCGAGCGATCGGCAGAGGAGAAGGGGCGGCTGGGAGACCTGTGGGTG  720
221  E  E  E  R  G  E  R  S  A  E  E  K  G  R  L  G  D  L  W  V   240
                             CD-X


721  TGAGCCTGGCCGTCCTCCGGGGCCACCGACCGCAGCCAGCCCCTCCCCAGGAGCTCCCCA  780


781  GGCCGCAGGGGCTCTGCGTTCTGCTCTGGGCCGGGCCCTGCTCCCCTGGCAGCAGAAGTG  840


841  GGTGCAGGAAGGTGGCAGTGACCAGCGCCCTGGACCATGCAGTTCGGCGGCCGCGGCTGG  900
```

901   GCCCTGCAGGAGGGAGAGAGAGACACAGTCATGGCCCCCTTCCTCCCTTGCTGGCCCTGA   960

961   TGGGGTGGGGTCTTAGGACGGGAGGCTGTGTCCGTGGGTGTGCAGTGCCCAGCACGGGAC   1020

1021 CCGGCTGCAGGGGACCTTCAATAAACACTTGTCCAGTAAAAAAAAAAAAAAAAAA   1074

Sequence alignment — Figure 4A

```
                                          10          20          30          40          50
  1  M - - - - - G A W A M L Y G V S M L C V L D L G Q P S V V E E P C G P G K V Q N G S G N N T R C   mGITR.aa
  1  M A Q H G A M G A F R A L C G L A L L C A L S L G Q R P T - - - - G G P G C G P G R L L L G T G T D A R C   TR11.aa
  1  M A P - G E R D S W - - - - - - I N P G P D S Q - P G A L C S L E P T V G G E R T T S L P   TR11SV1.aa
  1  M - - - - - G A F R A L C G L A L L C A L S L G Q R P T - - - - G G P G C G P G R L L L G T G T D A R C   TR11SV2.aa

                                          60          70          80          90         100
 45  C S L Y A - - - - - - - - - - - - - P G K E D C P K E R C I C V T P E Y H C G D P Q C K   mGITR.aa
 50  C R V H T T R C C R D Y P - - - - - - - - - G E E C C S E W D C M C V Q P E F H C G D P C C T   TR11.aa
 38  W R A E G R P G E E G A S A Q L L G G W P V S C P G E E C C S E W D C M C V Q P E F H C G D P C C T   TR11SV1.aa
 44  C R V H T T R C C R D Y P A Q L L G G W P V S C P G E E C C S E W D C M C V Q P E F H C G D P C C T   TR11SV2.aa

                                         110         120         130         140         150
 76  I C K H Y P C Q P G Q R V E S Q G D I V F G F R C V A C A M G T F S A G R D G H C R L W T N C S Q F   mGITR.aa
 88  T C R H P C P P G Q G V Q S Q G K F S F G F Q C I D C A S G T F S G G H E G H C K P W T D C T Q F   TR11.aa
 88  T C R H P C P P G Q G V Q S Q G K F S F G F Q C I D C A S G T F S G G H E G H C K P W T D C T Q F   TR11SV1.aa
 94  T C R H H P C P P G Q G V Q S Q G K F S F G F Q C I D C A S G T F S G G H E G H C K P W T D C T Q F   TR11SV2.aa

                                         160         170         180         190         200
126  G F L T M F P G N K T H N A V C I P E P L P T E Q Y G H L T V I F L V M A A C I F F L T T V Q L G L   mGITR.aa
138  G F L T V F P G N K T H N A V C V P G S P P A E P L G W L T V V L L L A V A A C V L L T S A Q L G L   TR11.aa
138  G F L T V F P G N K T H N A V C V P G S P P A E P L G W L T V V L L L A V A A C V L L T S A Q L G L   TR11SV1.aa
144  G F L T V F P G N K T H N A V C V P G S P P A E P L G W L T V V L L L A V A A C V L L T S A Q L G L   TR11SV2.aa
```

Figure 4A

```
              210        220        230        240        250
              |          |          |          |          |
176  H I W Q L R R Q H M C P R E T Q P F A E V Q L S A E D A C S F Q F P E E E R G E Q T - E E K C H L G   mGITR.aa
188  H I W Q L R K - - - R E T T Q L L E V P P S T E D A R S C Q F P E E E R G E R S A E E K G R L G   TR11.aa
188  H I W Q L R S Q C M W P R E T T Q L L E V P P S T E D A R S C Q F P E E E R G E R S A E E K G R L G   TR11SV1.aa
194  H I W Q L R K - - - R E T T Q L L E V P P S T E D A R S C Q F P E E E R G E R S A E E K G R L G   TR11SV2.aa


225  G R W P   mGITR.aa
231  D L W V   TR11.aa
238  D L W V   TR11SV1.aa
237  D L W V   TR11SV2.aa
```

Decoration 'Decoration #1': Shade (with solid black) residues that differ from TR11.aa.

Figure 4B

Figure 5
TR-11 Polypeptide Analysis

- Alpha, Regions - Garnier-Robson
- Alpha, Regions - Chou-Fasman
- Beta, Regions - Garnier-Robson
- Beta, Regions - Chou-Fasman
- Turn, Regions - Garnier-Robson
- Turn, Regions - Chou-Fasman
- Coil, Regions - Garnier-Robson
- Hydrophilicity Plot - Kyte-Doolittle
- Hydrophobicity Plot - Hopp-Woods
- Alpha, Amphipathic Regions - Eisenberg
- Beta, Amphipathic Regions - Eisenberg
- Flexible Regions - Karplus-Schulz
- Antigenic Index - Jameson-Wolf
- Surface Probability Plot - Emini

Figure 6

TR-11SV1 Polypeptide Analysis

A	▣ Alpha, Regions - Garnier-Robson
A	▤ Alpha. Regions - Chou-Fasman
B	▣ Beta, Regions - Garnier-Robson
B	▨ Beta. Regions - Chou-Fasman
T	▢ Turn, Regions - Garnier-Robson
T	■ Turn, Regions - Chou-Fasman
C	▫ Coil, Regions - Garnier-Robson
2.87 / 0 / -3.12	▨ Hydrophilicity Plot - Kyte-Doolittle
3 / 0 / -3.4	▫ Hydrophobicity Plot - Hopp-Woods
	■ Alpha, Amphipathic Regions - Eisenberg
	▨ Beta, Amphipathic Regions - Eisenberg
F	▨ Flexible Regions - Karplus-Schulz
3.4 / 0	▨ Antigenic Index - Jameson-Wolf
6 / 1	▫ Surface Probability Plot - Emini

Figure 7
TR-11SV2 Polypeptide Analysis

A — Alpha, Regions - Garnier-Robson
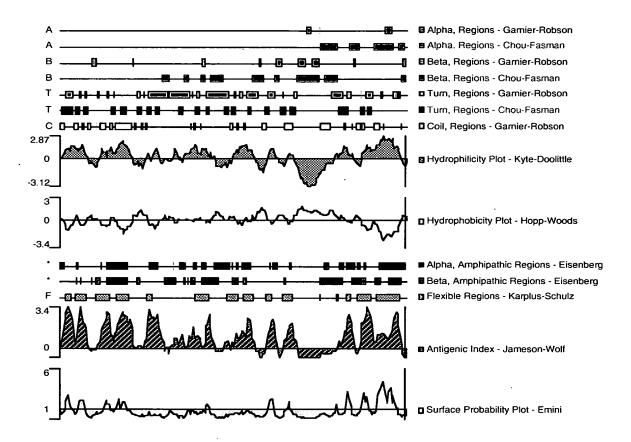A — Alpha, Regions - Chou-Fasman
B — Beta, Regions - Garnier-Robson
B — Beta, Regions - Chou-Fasman
T — Turn, Regions - Garnier-Robson
T — Turn, Regions - Chou-Fasman
C — Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
F — Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini